

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Boyle, William J.
- (ii) TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Amgen Inc.
 - (B) STREET: 1840 Dehavilland Drive
 - (C) CITY: Thousand Oaks
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 91230-1789
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Winter, Robert B.
 - (C) REFERENCE/DOCKET NUMBER: A-451D

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTTCTCCTCA TATGGATCCA AACCGTATTT CTGAAGACAG CACTCACTGC TT

52

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TACGCACTCC GCGGTTAGTC TATGTCCTGA ACTTTGA

37

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTTCTCCTCA TATGAAACCT GAAGCTCAAC CATTTGCACA CCTCACCATC AAT

53

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTTCTCCTCA TATGCATTTA ACTATTAACG CTGCATCTAT CCCAT

45

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTTCTCCTCA TATGACTATT AACGCTGCAT CTATCCCATC GGGTTCCCAT AAAGTCACT

59

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 158..1105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | | | |
|---|-----------------|------------|------------|-------------------------|------------|-----|
| GAGCTCGGAT | CCACTACTCG | ACCCACGCGT | CCGGCCAGGA | CCTCTGTGAA | CCGGTCGGGG | 60 |
| CGGGGGCCGC | CTGGCCGGGA | GTCTGCTCGG | CGGTGGGTGG | CCGAGGAAGG | GAGAGAACGA | 120 |
| TCGCGGAGCA | GGGCGCCCGA | ACTCCGGGCG | CCGCGCC | ATG CGC CGG GCC AGC CGA | 175 | |
| | | | | Met Arg Arg Ala Ser Arg | | |
| | | | | 1 5 | | |
| GAC TAC GGC AAG TAC CTG CGC AGC TCG GAG GAG ATG GGC AGC GGC CCC | 223 | | | | | |
| Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro | | | | | | |
| | 10 15 20 | | | | | |
| GGC GTC CCA CAC GAG GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT | 271 | | | | | |
| Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala | | | | | | |
| | 25 30 35 | | | | | |
| CCG GCG CCG CCA CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG | 319 | | | | | |
| Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu | | | | | | |
| | 40 45 50 | | | | | |
| GGG CTG GGA CTG GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC | 367 | | | | | |
| Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr | | | | | | |
| | 55 60 65 70 | | | | | |
| TTT CGA GCG CAG ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC | 415 | | | | | |
| Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His | | | | | | |
| | 75 80 85 | | | | | |
| TGC TTT TAT AGA ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC | 463 | | | | | |
| Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp | | | | | | |
| | 90 95 100 | | | | | |
| TCG ACT CTG GAG AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG | 511 | | | | | |
| Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met | | | | | | |
| | 105 110 115 | | | | | |
| AAA CAA GCC TTT CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG | 559 | | | | | |
| Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val | | | | | | |
| | 120 125 130 | | | | | |
| GGG CCA CAG CGC TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG | 607 | | | | | |
| Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp | | | | | | |
| | 135 140 145 150 | | | | | |
| TTG GAT GTG GCC CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC | 655 | | | | | |
| Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His | | | | | | |
| | 155 160 165 | | | | | |
| CTC ACC ATC AAT GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT | 703 | | | | | |
| Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr | | | | | | |
| | 170 175 180 | | | | | |
| CTG TCC TCT TGG TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG | 751 | | | | | |
| Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser Asn Met | | | | | | |
| | 185 190 195 | | | | | |
| ACG TTA AGC AAC GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC | 799 | | | | | |
| Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr | | | | | | |
| | 200 205 210 | | | | | |

| | | | | | | | | | | | | | | | | |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|----------------------------------|-------------------|-------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| CTG Leu 215 | TAC Tyr | GCC Ala | AAC Asn | ATT Ile | TGC Cys 220 | TTT Phe | CGG Arg | CAT His | CAT His | GAA Glu 225 | ACA Thr | TCG Ser | GGA Gly | AGC Ser | GTA Val 230 | 847 |
| CCT Pro | ACA Thr | GAC Asp | TAT Tyr | CTT Leu 235 | CAG Gln | CTG Leu | ATG Met | GTG Val | TAT Tyr 240 | GTC Val | GTT Val | AAA Lys | ACC Thr | AGC Ser 245 | ATC Ile | 895 |
| AAA Lys | ATC Ile | CCA Pro | AGT Ser 250 | TCT Ser | CAT His | AAC Asn | CTG Leu 255 | ATG Met | AAA Lys | GGA Gly | GGG Gly | AGC Ser | ACG Thr 260 | AAA Lys | AAC Asn | 943 |
| TGG Trp | TCG Ser | GGC Gly 265 | AAT Asn | TCT Ser | GAA Glu | TTC Phe | CAC His 270 | TTT Phe | TAT Tyr | TCC Ser | ATA Ile | AAT Asn 275 | GTT Val | GGG Gly | GGA Gly | 991 |
| TTT Phe | TTC Phe 280 | AAG Lys | CTC Leu | CGA Arg | GCT Ala | GGT Gly 285 | GAA Glu | GAA Glu | ATT Ile | AGC Ser | ATT Ile 290 | CAG Gln | GTG Val | TCC Ser | AAC Asn | 1039 |
| CCT Pro 295 | TCC Ser | CTG Leu | CTG Leu | GAT Asp | CCG Pro 300 | GAT Asp | CAA Gln | GAT Asp | GCG Ala | ACG Thr 305 | TAC Tyr | TTT Phe | GGG Gly | GCT Ala | TTC Phe 310 | 1087 |
| AAA Lys | GTT Val | CAG Gln | GAC Asp | ATA Ile 315 | GAC Asp | TGAGACTCAT TTCGTGGAAC ATTAGCATGG | | | | | | | | | | 1135 |
| ATGTCCTAGA | | | | TGTTTGAAA | | CTTCTTAAAA | | AATGGATGAT | | | GTCTATACAT | | GTGTAAGACT | | | 1195 |
| ACTAAGAGAC | | | | ATGGCCACG | | GTGTATGAAA | | CTCACAGCCC | | | TCTCTCTTGA | | GCCTGTACAG | | | 1255 |
| GTTGTGTATA | | | | TGTAAGTCC | | ATAGGTGATG | | TTAGATT CAT | | | GGTGATTACA | | CAACGGTTTT | | | 1315 |
| ACAATTTTGT | | | | AATGATTTCC | | TAGAATTGAA | | CCAGATTGGG | | | AGAGGTATTC | | CGATGCTTAT | | | 1375 |
| GAAAACTTA | | | | CACGTGAGCT | | ATGGAAGGGG | | GTCACAGTCT | | | CTGGGTCTAA | | CCCCTGGACA | | | 1435 |
| TGTGCCACTG | | | | AGAACCTTGA | | AATTAAGAGG | | ATGCCATGTC | | | ATTGCAAAGA | | AATGATAGTG | | | 1495 |
| TGAAGGGTTA | | | | AGTTCTTTTG | | AATTGTTACA | | TTGCGCTGGG | | | ACCTGCAAAT | | AAGTTCTTTT | | | 1555 |
| TTTCTAATGA | | | | GGAGAGAAAA | | ATATATGTAT | | TTTTATATAA | | | TGTCTAAAGT | | TATATTT CAG | | | 1615 |
| GTGTAATGTT | | | | TTCTGTGCAA | | AGTTTTGTAA | | ATTATATTTG | | | TGCTATAGTA | | TTTGATTCAA | | | 1675 |
| AATATTTTAA | | | | AATGTCTCAC | | TGTTGACATA | | TTTAATGTTT | | | TAAATGTACA | | GATGTATTTA | | | 1735 |
| ACTGGTGCAC | | | | TTTGTAATTC | | CCCTGAAGGT | | ACTCGTAGCT | | | AAGGGGGCAG | | AATACTGTTT | | | 1795 |
| CTGGTGACCA | | | | CATGTAGTTT | | ATTTCTTTTAT | | TCTTTTTTAAC | | | TTAATAGAGT | | CTTCAGACTT | | | 1855 |
| GTCAAAACTA | | | | TGCAAGCAAA | | ATAAATAAAT | | AAAAATAAAA | | | TGAATACCTT | | GAATAATAAG | | | 1915 |
| | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Arg | Arg | Ala | Ser | Arg | Asp | Tyr | Gly | Lys | Tyr | Leu | Arg | Ser | Ser | Glu | 1 | 5 | 10 | 15 |
| Glu | Met | Gly | Ser | Gly | Pro | Gly | Val | Pro | His | Glu | Gly | Pro | Leu | His | Pro | 20 | 25 | 30 | |
| Ala | Pro | Ser | Ala | Pro | Ala | Pro | Ala | Pro | Pro | Pro | Ala | Ala | Ser | Arg | Ser | 35 | 40 | 45 | |
| Met | Phe | Leu | Ala | Leu | Leu | Gly | Leu | Gly | Leu | Gly | Gln | Val | Val | Cys | Ser | 50 | 55 | 60 | |
| Ile | Ala | Leu | Phe | Leu | Tyr | Phe | Arg | Ala | Gln | Met | Asp | Pro | Asn | Arg | Ile | 65 | 70 | 75 | |
| Ser | Glu | Asp | Ser | Thr | His | Cys | Phe | Tyr | Arg | Ile | Leu | Arg | Leu | His | Glu | 85 | 90 | 95 | |
| Asn | Ala | Gly | Leu | Gln | Asp | Ser | Thr | Leu | Glu | Ser | Glu | Asp | Thr | Leu | Pro | 100 | 105 | 110 | |
| Asp | Ser | Cys | Arg | Arg | Met | Lys | Gln | Ala | Phe | Gln | Gly | Ala | Val | Gln | Lys | 115 | 120 | 125 | |
| Glu | Leu | Gln | His | Ile | Val | Gly | Pro | Gln | Arg | Phe | Ser | Gly | Ala | Pro | Ala | 130 | 135 | 140 | |
| Met | Met | Glu | Gly | Ser | Trp | Leu | Asp | Val | Ala | Gln | Arg | Gly | Lys | Pro | Glu | 145 | 150 | 155 | |
| Ala | Gln | Pro | Phe | Ala | His | Leu | Thr | Ile | Asn | Ala | Ala | Ser | Ile | Pro | Ser | 165 | 170 | 175 | |
| Gly | Ser | His | Lys | Val | Thr | Leu | Ser | Ser | Trp | Tyr | His | Asp | Arg | Gly | Trp | 180 | 185 | 190 | |
| Ala | Lys | Ile | Ser | Asn | Met | Thr | Leu | Ser | Asn | Gly | Lys | Leu | Arg | Val | Asn | 195 | 200 | 205 | |
| Gln | Asp | Gly | Phe | Tyr | Tyr | Leu | Tyr | Ala | Asn | Ile | Cys | Phe | Arg | His | His | 210 | 215 | 220 | |
| Glu | Thr | Ser | Gly | Ser | Val | Pro | Thr | Asp | Tyr | Leu | Gln | Leu | Met | Val | Tyr | 225 | 230 | 235 | |
| Val | Val | Lys | Thr | Ser | Ile | Lys | Ile | Pro | Ser | Ser | His | Asn | Leu | Met | Lys | 245 | 250 | 255 | |
| Gly | Gly | Ser | Thr | Lys | Asn | Trp | Ser | Gly | Asn | Ser | Glu | Phe | His | Phe | Tyr | 260 | 265 | 270 | |
| Ser | Ile | Asn | Val | Gly | Gly | Phe | Phe | Lys | Leu | Arg | Ala | Gly | Glu | Glu | Ile | 275 | 280 | 285 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ile | Gln | Val | Ser | Asn | Pro | Ser | Leu | Leu | Asp | Pro | Asp | Gln | Asp | Ala |
| 290 | | | | | | 295 | | | | | 300 | | | | |
| Thr | Tyr | Phe | Gly | Ala | Phe | Lys | Val | Gln | Asp | Ile | Asp | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | |

2024-04-24